

# FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT  
 GTTGAAGGGTGTTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG  
 TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA  
 CTACTCTCTTCTGACAGTCTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG  
 CTCCTATTATTTCTGGCTTTTGTGCTCTGCCAAACCCTTCTTAGCCCTTCACACATCGCAT  
 GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG  
 ATGATGATGATGAGGACAACTCTCTTTTCCAAACAAGAGAGCCAAGAAGCCATTTTTCCTCA  
 TTTGATCTGTTTTCCAATGTGTCCATTGGATGTGAGTGCTATTACGAGTTGTACATGTCTC  
 AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTTGATCTCGAATGCTTGATCTTC  
 AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT  
 CTGATCCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTTCTAACCAAAAGAA  
 GTTGCGAAGGCTGTATCTGTCCACAATCAACTAAGTGAAATACCACTTAATCTTTCCCAAT  
 CATTAGCAGAACTCAGAATTCTATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAA  
 GGAATGAATGCTTTACACGTTTGGAAATGAGTGCAAACCCCTCTTGATAATAATGGGATAGA  
 GCCGAGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATGCAGAAAGCAAACTGACCT  
 CAGTTCTTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA  
 ACAGTGGAACTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA  
 CAAAATCAGAGATATCGAAAATGGGAGTCTTGCTAACATACCAGCTGTGAGAGAAATACATT  
 TGGAAAACAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA  
 ATCTTCCTTCACTTAATTCAATTGCAAGAGTGGGAGTAAATGACTCTCTGTCCAACAGTGCC  
 AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACCAACCCGGTGAAATACCTGGG  
 AAATGCAACCTGCAACATTTCGTTGTGTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACCTT  
 GGAATGTAATAAATAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT  
 TGGAAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAAATATCTATTCTCA  
 AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT  
 GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTCGCTACAAATGAT  
 CTTACATAAACTCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTA  
 TTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGACTTAAATGGAAATGCTTGACT  
 TAGCAAAATTTGTGCTCTTTTCATTGTGCTGTAGAAAAACAGAATTAACAAAGACAGTAATGT  
 GAAGAGTGCACTACACTATTTCTTATTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAAT  
 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTAACCTATCATGTCTTAGAGCCCGT  
 CTTTATGTTTTAAACTAAATTTCTTAAATAAAGCCTTCAGTAAATGTTTCATTACCAACTTGA  
 TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATATT  
 ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACCTCGCATTTT  
 AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC  
 TTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAGAGAGCTGGA  
 CACTACAATTTACACCAAAATGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA  
 CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA  
 TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAATCAGAAA  
 ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAT

## **FIGURE 2**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR  
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL  
TSLYGLILNKNKLTIKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ  
KDTFKGMNALHVLEMSANPLDNNGIEPGAEGVTVPFHIRIAEAKLTSVPKGLPPTLLELHLD  
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLNENKLLKIPSGLPPEL  
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV  
QLGNFGM

### **Signal sequence.**

amino acids 1-15

### **N-glycosylation site.**

amino acids 281-285

### **N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

### **Leucine zipper pattern.**

amino acids 154-176

# FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCCGCGCACCGCCCCGCGCCGCCCTCCGCGCTCCGCACTCGCGCCTCC  
 CTCCTCCGCGCCGCTCCGCGCGCTCTCCCTCCCTCCCTCCCAAGCTGTCGCGGTTCGCGCTC**ATG**CGCGAGCCTCCC  
 GGCCCGCGCGCGCCGCTGCTGCTCTCTGGGCTGCTGCTGCTCGGGCTCCCGGCGCGCGCGCGCGCGCGCGAG  
 GCGCCCGCTGCTGCCCATCGTTCTTGAGAAGGAGCGCTGCCGTTTGGGGAGCGGCAAGGCTGCACCTTCGGCGG  
 GAAGGTCTATGCTTGGACAGGACGTGCGACCCGGACCTAGGGCAGCGATTGGGGGTGATGCGCGTGCCTGCTGTG  
 CGCTGCGAGGCGCTCAGTGGGGTTCGCCGTACCAAGGGCCCTGGCAGGCTCAGGTGACGTGCAAGAATCAAAACAGA  
 GTGCCAAACCCCGGCTGTGGGCAGCGCGCGCAGCTGCCGGGACACTGCTGCCAGACCTCGCCCCAGGAGCGCAG  
 CAGTTCCGAGCGCGCAGCGGAGCGGCTGTCTTCAGATATCCGCGGACCTCCGAGCATCGCAATTATAGCCACCG  
 CGGGGAGCCAGGCGCTGAGGAGCGGGCCGTTGGTACGGGCCACACGGGCTTCGTGGCGCTGCTGACAGGGCCGAG  
 GTCGACGGCGGTGGGACAGGCGCGAGTCTCGCTGCTGCGCTCTAGGCTCCGCTTCTTATCTCCTACAGGCGGCT  
 GGACCGCCTACCAAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTGGAGCACCTGCGAGCGCCACCCA  
 AGATGGCCTGGTCTGTGGGTGTGGCGGCGAGTGCCTCGGTTGTCTCTCGCGCTCCTTAGGGCAGAACAGTGCAC  
 TGTGGCACTTGTGACACTCACTCACCTTACGGGAGGCTCTGGGGCTCTCATCCGGCACCGGGGCTGTGCTGC  
 AGAGACCTTCAGTGCCATCCTGACTTAGAAGGCGCCCAACAGCAGGGCGTAGGGGGCATCACCTTGCTCACTCT  
 CAGTGACACAGAGGACTCCTTGCAATTTTGTGCTCTTCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC  
 CCAGGTTCCCTTGAGGCTTCAGATTCTACACCAAGGGGAGCTACTGCGAAGACTTCAGGCCAATGTCTCAGCCCA  
 GGAACCAAGGCTTTGCTGAGGTGTGCCAACCTGACAGTCCAGGAGATGAGCTGGCTGGTCTGGGGGAGCTGCA  
 GATGGCCCTGGAGTGGCGAGCGAGCGAGGCTGGGCATCAGTGGACACATGCTGCGCAGGAAGAGCTCGACGT  
 CCTGCAAAAGTGTCTTTGTGGGGCTGATGCCCTGATCCAGTCCAGACGGGTGCTGCCGGCTCAGCCAGCCTCAC  
 GCTGCTAGGAAATGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAAGTGGTGGCCATGACACT  
 GGAGACCAAGCTCAGCGGAGGGATCAGCGCACTGTCTGTCACATGGCTGGACTCAGGACAGGAGGACACAT  
 GGCGGTGGGTATCTGCCCTGGGTGGGTGCCCGAGGGGCTCATATGCTGCTGCAGAAAGAGCTCTTCCTGAACGT  
 GGGCAACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCGACGTGGCTGCCCTGCTGCTGCTGCTGGGCGATGCGCCG  
 CCATGACACGCTGCCCGTGCCCTAGCAGGAGCCCTGGTGTCTACCCCTGTGAAGAGCCAAAGCAGCAGGGCACGC  
 CTGGCTTTCCTGGATACCCACTGTCACTCGCACTATGAAGTGTGCTGGCTGGGCTTGGTGGCTCAGAACAGG  
 CACTGTCACTGCCCCACTCTCTGGGCTCTTGGAAACGCCAGGGCTCGGGCGGCTGCAAGGGATCTATGAGCTC  
 AGAGGCCCGAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTCTGCGCGCACTTGGCAAAAGGCGATGGCCTCCCTGAT  
 GATCACCAACAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATGCCAACCAATGTGAGGTGGCGG  
 ACTGCGCTGGAGGCGCGCGGGGCGAGGGGCTGCGGGCGCTGCGGGCTCCGGATACAGCTCTGCTGCGCGCGC  
 TGTGTGCTGCTGCTCCCGGCCCTAGCGCCCGCACAACTGGTGTCTTGGGCGCGCCCGAGACCCCAACCATG  
 CTTCTCGAGGGGCGAGCGCGCCCCACGGGGCTCGTGGGCGGCCAACTACGACCCGCTCTGCTCACTCTGCAC  
 CTGCCAGAGACGAAGGTGATCTGTGACCCGTTGGTGTGCCCACTGCCAGCTGCCACACCCGGTGCAGGCTCC  
 CGACCAGTGTCTGCCCTGTTTGGCTGAGAAACAAGATGTACAGACTTGGCAGGGCTGCCAAGGAGCCGGGACCC  
 AGGAGAGGGTGTCTATTTTGATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCC  
 CTTTGGCTTAATTAAGTGTGCTGTCTGCACCTGCAAGGGGGGCACTGGAGAGTGCACGTGTGAGAAGGTGCAAGT  
 TCCCCGGCTGGCTGTGCCAGCTGTGCTGTCAACCCCAACGACTGCTGCAAAAGTGTCCAGTGGGGTGGG  
 GGCCACCCCCAGCTGGGGGAGCCCATGCAAGCTGATGGGCCCCGGGGCTGCCGTTTGGCTGGGCAAGTGGTCCC  
 AGAGAGTCAGAGTGGACACCCCTCAGTGCCTCTTTTGGAGAGATGAGCTGTATCAGCTGCAGATGTGGGCGAGG  
 GGTGCTCACTGTGAGCGGATGACTGTTCACTGCCACTGCTCTGTGCTCGGGGAAGGAGAGTGCATGCTGTT  
 CGCTGTCAGCGCCCAAGCGGCCCCCAGAGACCAAGACTGATCCAGAGTGGAGAAAGGCGAAGGCTCT**TA**  
 GGGAGCAGCCAGAGGGCCAAGTGACCAAGAGATGGGGCTGAGCTGGGGAAAGGGTGGCATCGAGGACCTTCTT  
 GCATTCTCCTGTGGGAAGCCAGTGCTCTTGCTCTCTGTCTGCTCTACTCCCAACCCCACTACCTCTGGGAA  
 CCACAGCTTCCAAAGGGGAGAGCGAGCTGGGCGACAGCGAGTCAAGCCATCTCAAGTCTCGCTGCCACCT  
 TGGGCTCTGTCTGGAAGCCCCACCTTCTCTCTGTACATAATGTCACTGGCTGTGTGGGATTTTAATTTA  
 TCTTCACTACGACCAAGGGCCCCCGGACACTCCACTCTGCTGCCCTGAGCTGGCAGAGTCATTATTGGAGAG  
 TTTTGTATTATTAAACATTTCTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLGLLLSGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE  
TWHPDLGQPPFGVMRCVLCACEAPQWGRRTRGPGRVSCNLIKPECPTACGQPRQLPGHCCQT  
CPQERSSSERQPSGLSFYPRDPEHRYSYSDRGEPGAEERARGDGHDTDFVALLTGPRSQAVAR  
ARVSLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEPHAAPTQDGLVCGVWRAVPRLSLRL  
LRAEQLHVALVTTLTHPSGEVWGPLIRHRAAAETPSAILTLEGPPQQGVGGITLLTSDTED  
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPNLTQVEMD  
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALI PVQTGAAGSASLTLLGN  
GSLIYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML  
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS  
LDTHCHLHYEVLLAGLGGSEQGTVTAHLLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGLRLEAAGAEGVRALGAPDTASAAPPVV  
PGLPALAPAKPPGGPRPRDPNTCFEFGQQRPHGARWAPNYDPLCSLCTCQRRRTVICDPVVC  
PPSCPHVPQAPDQCCPVCPEKQDVRDLPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPF  
GLIKCAVCTCKGGTGEVHCEKQVQCPRLACAQPVVRNPTDCCQCPVGSAGHPQLGDPMQADG  
PRGCRFAGQWFPESQSWHPSVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCSGSKESRCCS  
RCTAHRPPETRTDPELEKEAEGS

### Signal sequence.

amino acids 1-23

### N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

### Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

### N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

### Amidation site.

amino acids 87-91

### Cell attachment sequence.

amino acids 165-168

### Leucine zipper pattern.

amino acids 315-337

## FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCGCCGCCGCTCACTGCG  
TCTTGCTCCGCTCCCGCGCCCTCCCGCGCGGC**CATG**CAGCCCCGCCCGCGCCAGCGCCCGGTTGCGCAGCTGCG  
TGCCCGCGCTGCGCCCTGCTGTGCTGTGCTCGGAGCGGGGCCCGAGCAGCTCCCTTGCCCAACCCGGTGGCCG  
CGCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGAATAGGGGTGTGTGCACCTCGCGCCCTG  
AGCCGGACCGCGAGCACCAGCGCCCGCGCGCGGAGCCTGGCTACAGCTGCACCTGCCCGCGCGGATCTCCGCG  
CCAACTGCCAGCTTGTGTGAGATCTTGTGCCAGCAACCCCTTGTCCAGAGTGCACCTGCGAGCAGCAGCAGCA  
GCAGCAGCAGTGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGCAGCATTCCCGAGTC  
TCCAGCGATGCTGGAGCCGAATCCATGGCACCCCGACAGCTTCAGCCTGTCTCTGCTAGCTCAGGAGCCTTGACA  
AAATCTGCGCTCGCTCTCAGGCAACGGTGCACCTGCCTACCTGGCAGCCGAAACAGGGCGAGAAGTTGTAGAAA  
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGACC  
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTGCGCAAGATGCCACTGCCTCCTCAGCTGATT  
TCTGGAAGGTCAAGCGCACAGGATTCCAACAGTGTCCCTCATAGATGGACGAAGTGTGACCCCTTCAAGCTT  
CAGGGGACTGGTCTCTCGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG  
TGACTAAGTCTATTGTGGCTTTTGGCTTAACTCTGGTGGTGAAGGTGACAGCTGTGTGCCGGGGAGAGTCAGC  
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGCAACTTTTCTCTGTAACCTGTG  
AGGAGCAGTACCTGGGTACTTTTCTGTGAAGAAATACGATGCTTGGCAGAGGAACCTTGCCAAAACACCGGAGCT  
GTAATTCGACAAATGAAAGCAAGATGGGAGCAATTTCACTGTGTTTGCCTTCTGGTTATAGTGGAGAGCTTT  
GCCAGTCCAGATTGATTACTGCTAGTCCATGACCCATGCAGAAATGGAGCAACATGCATTTCCAGCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT  
GCCAGAACACCGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA  
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCCCTGTGCTCATGGCAGCTGCCGAGCTGGGGCACAGCT  
ACAAATGCTCTGTGATCAGGTTACCATGGCCTCTACTGTGAGAGGAATATAATGAGTGCCTCTCCGCTCCAT  
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGATGTGTGTGCTGCTGGCAGAAATACAAAGGAACAC  
ACTGTGAATTTGACAGGATCCCTGCGCTAACGTCAGCTGTCTGAACGGAGCCACCTGTGACAGCAGCGGCTTGA  
ATGGCAGCTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCACATTGACATAAATGAATGTGACAGTAAAC  
CCTGCCACCATGGTGGGAGCTGCTGGACCAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG  
CAAACTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGSCGGAGAGCCTCACCACATGCGCAGGCACTCCC  
TCTACATCATCATTGGAGCCCTCTGGTGGCCTTATCCTTATGCTGATCATCCTGATCGTGGGGATTTCGCGCA  
TCAGCCGATTGAATACCAAGGTTTCTTCAGGCCAGCCTATGAGGAGTTCTACAACCTGCCGAGCATCGACAGCG  
AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGTTTGGAAAAGAAATCCCGGCTGCAATGTATGATGTGA  
GCCCCATCGCCTATGAAGATTACAGCTCTGATGACAAACCTTGGTCACTGATTAAAACTAAAGATTGT**TAAT**  
CTTTTTTTGGATTATTTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTAAAGAAAATAAAAGCTTAA  
GAAATTTAAATAGCTAGCTGCTCAAGAGTTTTCAGTAGAATATTTAAGAAATAAATTTCTGAGCTTTTAGTTTG  
GAAAAATATTTTAAAAACAATAATTTGTGAAACCTATAGACGATGTTTAAATGACCTTCAGCTCTCTAAACTGT  
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAAATTTCTGTGGTTGTGACA  
GAATAAGCTTAATCAAGGAGAAGTTTCTGTTTGACGTTTGAGTGCCGGCTTCTGAGTAGAGTTAGGAAAACCA  
GTAACTAGCATATGATGTATAATAGATGATACCCGTTACTTAAAGAAAGCTTGAATGTCTGTTTGTGGAAA  
AGAAACTAGTTAAATTTACTATCTTCAACCCGAATGAAATTAGCCTTTGCGCTTATTCTGTGCTGGGTAAAGTAA  
TTATTTCTGCACTGTTTGTGTAACCTTTGTGAAACATTCTTCGAGTTTGTGTTTGTGCTTTTGTGCTTAACTG  
TCGAATCAAGCCTCAAAAACATACGTAAACGAAAAGCCCTGACGAGGCAATCTGATTGTTTGAATGTATATT  
TCTTTTAAAGTCAAGGTTTCTATATTGTGAGTAAATTAATTTACATTGAGTTGTTTGTGCTAAAGAGGTAG  
TAAATGTAAAGAGTACGGTTCCTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTATCTCCAGGATGTT  
TTTGTGGCTGATTGTTGATATGTGCTTCTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC  
AGGTCA

0944866.083104

## FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANFPVPAAPLSAPGPCAAQPCRNGGVCTSR  
PEPDPQHPAPAGEPGYSCTCPAGISGANCLVADPCASNPCHHGNCSSSSSSSSDGYLCICN  
EGYEGPNCQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGfq  
QCSLIDGRSVTPQLQASGGLVLEEMLALGNNHFIGFVNDSTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTTKPSEATFSCCTEEQYVGTFCCEEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKIDYCIIDPCRNATCISLSSGFTQCCEGYFGSACEEKVDPC  
ASSPCQNNGTCTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSTYKCLCDPG  
YHGLYCEEYNECLSAPLNAATCRDLVNGYECVCLAEYKGTHCELYKDPKANVSCLNGATC  
DSDGLNGTICAPGFTGEECDIDINECDSNPCHGGSCLDQPNGYNCHCPHGWWGANCEIHL  
QWKSGHMAESLTNMPRHSlyIIIGALCVAFILMLIILIVGICRISRIEYQGSRRPAYEEFYN  
CRSIDSEFSNAIASIRHARFGKSRPAMYDVSPITAYEDYSPDDKPLVTLLIKTKDL

### Signal sequence.

amino acids 1-28

### Transmembrane domain.

amino acids 641-660

### N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

### Glycosaminoglycan attachment site.

amino acids 320-324

### Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

### N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

### Amidation site.

amino acids 702-706

### Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

### EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

## **FIGURE 7**

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAAGTGTGA  
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC  
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC  
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

## **FIGURE 8**

CTCTGGAAGGTCACGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCTTTTCAGGCTTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT  
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTTGCCTTCC  
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG



## FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCTACACACGCCAG  
GCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCACACCATGCCGGGCACCTAC  
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT  
GATGCGGGACTTCCCCTCGTGGACGGCCACAACGACCTGCCCTTGGTCTTAAGGCAGGTTT  
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTACGTACGGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT  
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCTGGGCAGAGA  
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC  
GGGGTGTGTGCAACAGTGTGCGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC  
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGAACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCAATTGGATCCAAGTTCATCGGGA  
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATAC  
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT  
TCGTGGAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC  
AAAGCCCCTGGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCTTGCCACTCCGACCTC  
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACA  
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG  
TCCTTGCAAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC  
TGCCAGATGTCACTGTAGCAAGCCACAGACCCCCACAAAGTTCCCTGTGTGTCAGGCACA  
AATATTCTCTGAAATAAATGTTTTGGACATAG

## **FIGURE 10**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNNGGVVMVLSMGIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE  
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS  
CHSDLSRLRQRQSLTSGQELTEIPHWAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

### **N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

### **N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

### **Renal dipeptidase active site.**

amino acids 134-157

## FIGURE 11

AAAACTATAAATATTCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG  
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA  
CCAGGGCCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC  
AACGACCTGCCCTGGTCTTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTTAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCATG  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCCCTGGAG  
CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC  
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGTGTCTCGGAATGTTCC  
TGATGACATCCTGCACTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG  
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC  
AAGGCTGTCAATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAAAT  
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGAGTTGCTGAGTCGTG  
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCTCGTGGAACCTGTCTGCGGGTCTTCAGACAA  
GTGGAAAAGGTACAGGAAGAAAAAATAATGGCAAAGCCCTTGGAGGACAAGTTCCTCGGATGA  
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACCTCACTGAGATTCATACACTGGACAGCCAAAGTTACCAGCCAAGTGGTCA  
GTCTCAGAGTCCTCCCCCAACCTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGA  
ACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACAC

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE  
DVSTYPVLIEBLLSRGWSEELQGVLRGNLLRVFRQVEKVQEEKWQSPLEDKFPDEQLSSS  
CHSDLSRLRQRQSLTSGQELTEIP IHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP  
SVFLFPPKPKDT

10150, 500, 500, 500



## **FIGURE 14**

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLPLLLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTNLNGRRLLPELSRVLNASTLALALANLNGSRQSRGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSILKYKLRWYQDNTCEE  
YHTVGPCHSCHIPKDLALFTPYEIVWEATNRLGSARSDVLTLDILDVVTDDPPPDVHVS RVG  
LEDQLSVRVWVSPALKDFLFQAKYQIRYRVEDSVDWKVDDVSNQTSCLAGLKPGETVYFVQ  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSGPGVRRELKQFLG  
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

### **Signal sequence.**

amino acids 1-30

### **Transmembrane domain.**

amino acids 44-61

### **N-glycosylation sites.**

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 413-417

### **N-myristoylation sites.**

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

### **Amidation site.**

amino acids 3-7, 79-83, 411-415

### **Growth factor and cytokines receptors family signature 2.**

amino acids 325-331

## FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCCTCGTGAAGCTTTTTATTCTTAA  
GAGGAGAAAAATCAGTCACCGGCGAAAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTCATACCTTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA  
GGCATTCTCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
TCTGTGTCTCAATTTCTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGTTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAGGATCCTTCCTGAGCGTTT  
CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATTAAGCACCTAGTTTTCTGAAAACGATTTACCAGGTTTAGGTTGATGTCATCTA  
ATAGTGCCAGAATTTTAAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA  
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAAATACCTTTAGAGGTGACTTTAAGGAAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT  
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTTTCTGAGAGATACCTCACATTCCAATGCCAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

## **FIGURE 16**

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGVGHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKQA

### **Signal sequence.**

amino acids 1-19

### **Transmembrane domain.**

amino acids 170-187

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

### **N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216



## **FIGURE 17**

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGAGCCGGCAGGGAGCGAACCCAGGACTG  
GGGTGACGCGAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT  
GCGAGAGGACCCCGGCGTCCGGGCTCCCGGTCCAGCGCTATGAGGCCACTCCTCGTCTCTGC  
TGCTCCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC  
CCGGGCAACCCCGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGGCCGGGCCG  
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGCGAGGGCGGGA  
GGCCGGGACTGCCGGGACCTCGAGGGGACC CGGGCCGCGAGGAGAGCGGGACCCCGGGG  
CCCACCGGGCCTGCCGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC  
CGAGAGCCGGGTGCCTCCGCCGTCTGACGACCCTTGCCCTTCGACCGCGTGCTGGTGAACG  
AGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA  
ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGG  
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTCTGGTGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC  
TAGAAGGAGGGTGTGAGGCTGACAACCAAGTTCATCCAGGAGGGCTGGCCCCCTGGAATATT  
GTGAATGACTAGGAGGTGGGTAGAGCACTCTCCGTCTCTGCTGCTGGCAAGGAATGGGAAC  
AGTGCTGTCTGCGATCAGGTCTGGCAGCATGGGCGAGTGGCTGGATTTCTGCCCAAGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT  
GGGGTGCTCTCTCTCGGTCTCTGCTTCTCTGGATCCTCCCCACCCCTCTGCTCTGGG  
GCCGGCCCTTTCTCAGAGATCACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHSQGLPGRDGRDGRDGAPGAP  
GEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESrvPPPSDAPLP  
FDRVLVNEQGHYDAVTGKFTCQVPGVYFVAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSWDHSSPVFA

### **Signal sequence.**

amino acids 1-15

### **N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

### **Cell attachment sequence.**

amino acids 77-80

## FIGURE 19

CTCTTTTGTCCACCAGCCAGCCTGACTCCTGGAGATTTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCTTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG  
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCTTGCACAACCGCCTGCGCAGCTGGGTCCA  
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG  
CAAGTGGGCTGGAACTGCAGCTGCTGCCCGGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG  
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCTGTGTTCGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCACCTGCAGTGTGTGC  
ACGGCCGGTTCCGGGAGGAGGAGTGTCTGTGCTCTGTGACATCGGCTACGGGGAGCCACAG  
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTTCAGAGGAAGGCG  
GGGTGCTGGCCAGATCAAGAGCCAGAAAAGTGACGGACATCCTCGCCTTCTATCTGGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGGCT  
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA  
GTTTTGCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT  
GGCAACTGCGTGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC  
CCGAAACCGTTACATCTGCCAGTTTGCCCGAGGACACATCTCCCGTGGGGCCAGGGTCTT  
GAGGGCCTGACCACATGGCTCCCTCGCTGCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA  
CCTTGACAAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTTAGAAGAAGCTGGGGCCCTTCGCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA  
TGGCAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCAGAC  
CCTGTGGGCAGCGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG  
CTGAAAAAAAAAAAAA

## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQA PMAGALNRKESFLLLSLHNLRSWV  
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSFGG  
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQCNHGRNLNISTCH  
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC  
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLLETTNEVTDSDFETRNFWIG  
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK  
TRNRYICQFAQEHISRWPGPS

### **Signal sequence.**

amino acids 1-26

### **Transmembrane domain.**

amino acids 110-124

### **N-glycosylation sites.**

amino acids 144-148, 243-247

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 45-49

### **N-myristoylation sites.**

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 204-215

### **EGF-like domain cysteine pattern signature.**

amino acids 249-261, 280-292

### **C-type lectin domain signature.**

amino acids 417-442

## FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAAGCGTGTCCCGCCGGTCCCCGAGCGTCCCGCGCCCT  
CGCCCCCGCATGCTCCTGCTGCTGGGGCTGTGCTGGGGCTGTCCCTGTGTGTGGGGTCGCA  
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG  
TCAGACTGTTGCAGAGGCTGAAAAACCAAACTTTGATGACAGAATTCTCAGTGAAGTCTACC  
ATCATTTCCTGTTATGCCTTCACTACGGTTCTCTGCAGAATGCTGAACAGAGCTTCTGAAGA  
CCAGGACATTGAGTTCAGATGACAGATCCAGCTGCAGCTTTTCATCACCAACTTCACTATGC  
TTATTGGAGACAAGGTGTATCAGGGCGAAAATTACAGAGAGAGAAAAGAGAGTGGTGATAGG  
GTAAAGAGAAAAAGGAATAAAACCAGAGAAGAAATGGAGAGAAGGGGACTGAAATATTCAG  
AGCTTCTGCAGTGAATCCCGCAAGGACAAAGCCGCTTTTCTCAGATTATGAGGAGCTTC  
TGCAGAGGCGCTGGGCAAGTACGAGCACAGCATCAGCGTGGCGCCCCAGCAGCTGTCCGGG  
AGGCTGAGCGTGGACGTGAATATCTTGGAGAGCGCGGCATCGCATCCCTGGAGGTGTGCGC  
GCTTCAACAACAGCAGGCAGAGGGGCGAGTGGGCGCGGGAAGATGATTCTGGGCTCCCCAT  
CTACTGTCTAATACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA  
CAAGCCAGGATTGCCAGAATGGAATTTTGGGAGACTTATCATTAGATATGACGTCAATAG  
AGAACAGAGCATTGGGGACATCCAGGTCTTAAATGGCTATTTGTGCACTACTTGTGCTCTA  
AAGACCTTCTCTTTTACCCAAGAAATGTGGTATTCGTGCTTGACAGCAGTGCTTCTATGGTG  
GGAACCAAACTCCGGCAGACCAAGGATGCCCTCTTCAAAATTCATGACCTCCGACCCCA  
GGACCGTTTCAGTATCATTTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT  
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGATACATTACCATATGTCAACCACTGGA  
GGCAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA  
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCACGG  
TCGGGGAGACGCACACCTCAAGATCCTCAACAACCCGAGAGGCGCCCGAGGCAAGTC  
TGCATCTTCAACATTGGCATCGGCAACGACGTGGAATTCAGGCTGTGGAGAACTGTGCT  
GGAGAACTTGGGCTCACACGGCGGTGCACGAGGAGGAGGACGAGGCTCGAGCTCATCG  
GGTTCTACGATGAAATCAGGACCCCGCTCTCTCTGACATCCGCATCGATTATCCCCCAGC  
TCAGTGGTGCAGGCCACCAAGACCTGTTCCTCAAACTACTTCAACGGCTCGGAGATCATCAT  
TGCGGGGAAGCTGGTGACAGGAAGCTGGATCACTTGACGTGGAGGTCAACGCCAGCAACA  
GTAAGAAATTCATCATCTTGAAGACAGATGTGCTGTGCGGCTCAGAAGGCAGGGAAGAT  
GTCACAGGAAGCCCCAGGCTGGAGGCGATGGAGAGGGGACCAACCACATCGAGCGTCT  
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGTCTCTGGCTGCAAAAGTGACGATGAACCGG  
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCC  
TTCACCTCCATGAAGCTGAGGGGGCCGGTCCACGCATGGATGGCTTGGAGGAGGCCACGG  
CATGTGCGGTGCCATGGGACCCGAACCGTGGTGTGCAGAGCGTGCAGGAGCTGACACGAGC  
CAGGACCTTTGCTCAAGAAGCCAACTCCGTCAAAAAAAAAACAAAACAAAAAAAGAGA  
CATGGGAGAGATGGTGTCTTCTCTCCACCCTGGGGATACGATGAGAAAGATGGCCACCT  
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGGACCTC  
CCAGCTCCAGAATGTGAGAAATAATGTGTTTTGTTTAAAGCTAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

CGGACGCGTGGGCTGGGCGCTGCAAAAGCGTGTCCCGCCGGTCCCCGAGCGTCCCGCGCCCT

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Y  
Z

&lt;MW: 77400, pI: 9.54, NX(S/T): 6

amino acids 1-14

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

## amino acids 213-217, 391-395

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGTCTGCCGAGCGGATCCACAGTGTGCGGC  
GGCAGCGGCGGCGGCGCCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG  
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTACAGTACTGAA  
TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGT  
TGCTGAATTTTTCTAGCAGTGAAGTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA  
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCAGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA  
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCAGTGATCTGCCAGGTGG  
AGCACCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGACACATTAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACTATCCCTCCTCCCAACAACACCACCACCA  
CCACCACCACCACCACCACCTTACCATCATCAGATTCCCAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCTGGCGGTGGTGGTGTTCGCCAT  
GCTGTGCTTGCTCATCATTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC  
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTTGTTTCAAT  
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

## **FIGURE 24**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAPGLRLLLLLFSAAALIP TGDGQNLF TKDVTVIEGEVATISC  
QVNSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQL  
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG  
KSEVEEWSDMYTVTSQMLKVHKEDDGVVPVICQVEHPAVTGNLQTQRYLEVQYKPOVHIQMT  
YPLQGLTREGDALELTCEAIGKPQPVMTWVRVDDMPQHAVLSGPNLFINNLNKTDNGTYR  
CEASNIVGKAHSDMYLVYDPPTTIPPPTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH  
AVIGGVVAVVVFAMLCLLIILGRYFARHKGYFTHEAKGADDAADADTAIINAEGGQNNSEE  
KKEYFI

### **Signal sequence.**

amino acids 1-36

### **Transmembrane domain.**

amino acids 372-393

### **N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

### **Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

### **N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432



## FIGURE 25

GGGGCGGGTGGACGCGGACTCGAAACGAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCCGA  
CCCCGCAGGAAAGACTGAGGCCGCGGCCCTGCCCCGCCGGCTCCCTGCGCCGCGCCGCCCTC  
CCGGGACAGAACTGTTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGCCCCT  
GGGGCTTGGGTGACAGGGCTGCCATCCGGCTGCAGTGCAGCCAGCCACAGACAGTCTTCT  
GCATGCGCCCGCAGGAGCCACCGTGCCCCGAGACGTGCCACCCGACACCGTGGGGCTGTAC  
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGGCTGCCGGGCTTGCA  
GCTCTGGACCTGTACAGAAACAGATCGCCAGCCTGCGCCTGCCCGCCCTGTGCTGCTGCG  
ACCTCGAGCCAAACAGCCTCCTGGCCCTGGAGCCCGCATCCTGGACACTGCCAACGTGGAG  
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTTCAGCCGCTTGCG  
CAACCTCCACGACCTGGATGTGTCCGACAAACAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
GCCTCCGGGGCTGCACGCGCTGCCGCTGCCCGGCAACACCCGATTGCCAGCTGCCGCC  
GAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC  
CCTGCCTGGCGACCTCTCGGGGCTCTTCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACC  
CCTTCAACTGCGTGTGCCCTTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTCACA  
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCGCCCAAGAACGCTGGCCGGCTGCTCCT  
GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACACAGCCACAGTGCCACCACCA  
CGAGGCCCTGGTGGCGGGAGCCACAGCCTTGCTTCTAGCTTGGCTCCTACCTGGCTTAGC  
CCACAGCGCCGGCCACTGAGGCCCCACGCCGCCCTCCACGCCCCACCGACTGTAGGCC  
TGTCCCCAGCCCCAGGACTGCCACCCTCCACCTGCCTCAATGGGGGCACATGCCACCTGG  
GGACACGGCACCACCTGGCGTGTGTGTGCCCGAAGGCTTACCGGCCCTGTACTGTGAGAGC  
CAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTACGCGCAGGGCCACCAGGTCCTT  
GACCTGGGCATCGAGCCGCTGAGCCCCACCTCCTGCGCGTGGGGCTGCAGCGCTACCTCC  
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT  
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGTGTAGTACACGGTCACCCAGCTGCG-  
GCCAACGCCACTTACTCCGCTGTGTGTATGCCTTTGGGGCCCCGGCGGGTGCCCGGAGGGCG  
AGGAGGCTTGGGGGAGGCCCATACCCCCAGCCGTCCTCAACCCAGCCCGAGTCAAC  
CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTTGCGCCGCCCTGGCCCGGCTGCTCCTGGC  
CGCGTGTGCGGTGGGGGAGCCTACTGTGTGCGCGGGGGCGGCCATGGCAGCAGCGG  
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTTGGAACTGGAGGGAGTGAAGGTC  
CCCTTGGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTTCCCGAGGGGTCTGA  
GTGTAGGTGCCACTCATGGCTTCCAGGGCCTGGCCTCAGTCAACCTCCACGCAAGC  
CCTACTCACTAAGCCAGAGAGAGACAGGGCAGCTGGGGCGGGCTCTCAGCCAGTGAGATGGC  
CAGCCCCCTCCTGTGCCACACCAGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA  
CAGGGCTGTGTGACCACAGCTGGGGCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG  
ATGCTGTGGCCAGCTGACGAGCCCTAACGTGCCCAAGACCGAGTGACCTATGAGGACAGTGT  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
GCATCCTGGGCCCTGTGGGCTCTCCCACTCCAGGCGGACCTTGGGGGCCAGTGAAGGAAG  
CTCCCGAAAGACAGAGGGAGAGCGGGTAGGGGCTGTGTACTGTAGTCTTGGCCCGAAG  
AAGCGAAGGAACAAAAGAACTGGAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA  
AATATATATATATTATAAGAGATCCTTTCCATTTATTTCTGGGAAGATGTTTTCAAAC  
AGAGCAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAAGGCCTTTTGTAAAGAAAA  
ATAAAAAAAAAA

## FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP LLLP LLL LLL LALGPGVQGCPSGCQSQPQT V FCTARQGT TVPRDVPD TVGLYVFEN  
GITMLDASSFAGLPGLQLDL SQNQIASLR LPR LLL LLDLSHNSLLALEPGILDTANVEALRL  
AGLGLQQLDEGLFSRLRNLHDLVDSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA  
GLAALQEELDVSNLSLQALPGDL SGLFPRLRL LLAARNPFNCVCPLSWFGPWWRESHVTLASP  
EETRCHFPFPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPT WLSPTAP  
ATEAPSPSTAPPTVGPVPQPD CPPSTCLNGGTCHLGRHHLACLCEPGFTGLYCESQMGG  
GTRPSPTPTVTPRPPRSLTLGIEFVSPTSLRVGLQRYLQSSVQLRSLRLTYRNLSGPDKRLV  
TLRLPASLA EYTTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGVGPAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFFPGPLQSP L HAKPYI

### Signal sequence.

amino acids 1-23

### Transmembrane domain.

amino acids 501-522

### N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

### Tyrosine kinase phosphorylation site.

amino acids 262-270

### N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

### EGF-like domain cysteine pattern signature.

amino acids 355-367

### Leucine zipper pattern.

amino acids 122-144, 194-216

## FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCTTACCCGCCCGCCACC  
TCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC**ATG**CCAGCCTC  
ATCTCCTTTCTTGCTAGCCCCAAAGGGCTCCAGGCAACATGGGGGCCAGTCAGAGAGC  
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC  
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC  
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGTTCCCATTAACGCCACCTCCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTAGGCGTGGGAGAGGCCCTAC  
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC  
CTGTTTCAAGACGTGACTTTCACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA  
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGACCGGGCTACAACAGCT  
GCTATAGCGCAGGTGTCTTCCATTACACCAAGGGGATATTCTGAGTGTATAATTCCCCGG  
GCAAGGGCGAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAACTG**TGA**TT  
GTGTTATAAAAAGTGGCTCCAGCTTGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA  
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC  
CCCGTTCCTCACTTTTCCCTTTTCATCCCCCCTAGACTTTGATTTTACGGATATCTTG  
CTTCTGTTCCCATGGAGCTCCG

## **FIGURE 28**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFL LAPKGP PGNMG GPVREP ALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV  
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRVLTQKQKKQHSVLHLVPIN  
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG  
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRRAKLNLSPHGTFLGFVKL

### **Signal sequence.**

amino acids 1-40

### **N-glycosylation site.**

amino acids 124-128

### **Tyrosine kinase phosphorylation site.**

amino acids 156-164

### **N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 34-45

## FIGURE 29

CACTTTCCTCCTCTCTTCTTACTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCGAGAGAC  
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA  
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTGT  
TCCTTTCACCGAGTCTGTGCATCGCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA  
TGCTCTAGGGGCGCGCGGGAGGAGCGCCCGCGGGAGCGAGGGCCCGGAGGAAGATGCGGC  
TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCTGCTCCTTGGCTTTGGCTCTGGCCTGGT  
CCTGAGTCTGTGCTCCCATCTGCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC  
CGTGCCTCTCCGAGCATCGGAGAGGGCTGAAGAACCAACATGA AAAATACAGGCCCATGACAG  
GACCAGGGGCTCCTGCTTCCCGGTGCTTGGCTGCTGTGACCCCGGTACCTCCATGTACCC  
GGCGACCGCCGTGCCCGAGATCAACATCACTATCTTGAAGGGGAGAGGGGTGACCGCGGAG  
ATCGAGGCCCTCCAAGGGAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA  
CCCAAGGGGCAGAAGGGCTCCATGGGGGCCCTTGGGAGCGGTGCAAGAGCCACTACGCCGC  
CTTTTCGGTGGGCCGGAAGAAGCCATGCAAGCAACCACTACTACCAGACGGTGATCTTCG  
ACACGGAGTTCGTGAACCTCTACGACCACCTTCAACATGTTACCCGGCAAGTCTTACTGTAC  
GTGCCCGGCTCTACTTCTTCAGCCTCAACGTGCACACCTTGAACCCAGAGGAGACCTTCT  
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCCGAGCA  
TCATGCAAAAGCCAGAGCTGTATGCTGGAGCTGCGAGAGCAGGACAGGTGTGGGTACGCCCTC  
TACAAGGGCGAAGCTGAGAACGCCATCTTACGCGAGGAGCTGGACACCTACATCACTTCAG  
TGGCTACCTGGTCAAGCAGGCCACCGAGCCCCTAGCTGGCCGGGCCACCTCTTTTCTCTGCC  
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCCTGGACTCCGACTC  
CCTGGCTTTGGCATTCTAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC  
CAGATCTCCGACGCTCTGGAGAGAGCTGACGGCAGATGAAATCACAGGGCGGGGACCCGCG  
GAGAACCTCTTGGGACTTCCGCGGCCCTCTCTGCACACATCTCAAGTGACCCCGCACGGC  
GAGACGGGGTGGCGGCAGGGCGTCCCAGGGTGGCGCACCCGCGCTCCAGTCTTGGAAATA  
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAAGTAAACCGTGGAGGACAAAGAAAAGG  
TTGTTATTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCCTTTTCAGTTGAG  
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGTGTCAGGGGAGGGGCCGGGGGAGG  
AAACTACTCTTGCTTAACTCTTTTAAAGCCACGTAGGAACCTTCTTGGAGGATAGGTGGAC  
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCAACAGTGCAGGT  
GATGGGGGCTGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCTTGGC  
TCCAGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA  
GGCCTGACAGATGTTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC  
ACCCCTGTGCCACCCAGAGCCCTGGGGGTGGTCTCCATGCTGCCACCCTGGCATCGGCT  
TTCGTGCGGCCCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT  
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTGCTGGCTAAGCATCACGGCT  
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCCT  
CATCCAGGCTCTGACAGTAGCCTGAGAGGGGCTTTTCTAGGCTTACAGAGCAGGGGAGAG  
CTGAAGGGGCTAGAAGCTCCCGCTTGCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTGT  
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCGTGTGAGGATTCACTCTCAGGAGC  
TGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCGAGGACAGCTGGAGCAGGGTTGCG  
GTGTCTCCACGGTGCTCTCGCCTGCCATGGCCACCCAGACTCTGATCTCCAGGAACCC  
ATAGCCCCCTCTCCACCTACCCCATGTGTGATGCCAGGGTCACTCTGTGCTACCGCTGGGCC  
CCCAAAACCCCGCTGCTCTCTTCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC  
TTCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT  
CTCGGGTCAAGCTCTGAAGCCGAGTTGTGTGGGCGTGCCCGGAGCAGAGCGCCACATC  
GCTGCTTAAGCTCCCCAGCTCTTTCAGAAAACATTAAACTCAGAAATGTGTTTTCAA

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP  
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH  
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFY  
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV  
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

### **Signal sequence.**

amino acids 1-25

### **N-glycosylation site.**

amino acids 93-97

### **N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

### **Amidation site.**

amino acids 150-154

### **Cell attachment sequence.**

amino acids 104-107

# FIGURE 31

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG  
GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA  
GAGAGAAATCTCATCATCTGTG CAGCCTTCTTAAAGCAAAC TAAGACCAGAGGGAGGATTAT  
CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTTCGGGGGAGAAGGGAG  
CTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTCAAAAAGAGTCTAGAAGATGTTGT CATTGACATCCAGT CATCTCTTTCTAAGGGAATC  
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATCTTGCTGTGTTCAAC  
AAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTA  
GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCCATCTTTGACCAGAAATTTGCCAAG  
CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAACAGCAGTCACTCCCC  
TAGCCCAATCATCACACAGATTATTCAAAGCCACCAGATATCTCATGGAGAGACACACTTTCT  
CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA  
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA  
TAGCTCATCTGCTGCCCTGAAATGTGAGTGCCTCCAGTACCGTGGCAGTTGCTTCTCCA  
CATACCACCTCGGCTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC  
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
AGCCTCCCACGACCCTCATTTCTACAGTTT TACAGGGCTGCGGTACACTCCAAGCAATG  
GCTACAACAGCAGTTCTGACTACCACTTT CAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
AACCATACGTTTACAGAAATCTCCAAC TTAACTTTGAACACAGGGAATGTGTATAACCCTA  
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCAGAAAATCAGTACGGCCCTTCC  
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGCTGATAGGCC  
TCGTCTCTCTGGGTAGAAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAAC TCGGTGTCTCTTAATTCATT  
TAGTAACCAAGAGCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
TATTTTGAAGACGAAAAATGCCCTTCTGCTTTCCTTTTTTTTTTGGAGACAGAGTCTT  
GCTCTGTTGCCAGCCTGGAGTG CAGTAGCACGATCTCGGCTCTCACCGCACCTCCGCTCTC  
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATACAGGCATGTGCCA  
CCACACCTGGGTGATTTTGTATTTT TAGTAGAGACGGGGTTTACCATGTTGGTCAGGCTG  
GTCTCAAACCTCTGACCTAGTGATCCACCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG  
CATGAGCCACCAAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTGAGAAGGAATGAAGTG  
GGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT  
ATGTAAGGTAATAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCATCTTGGTTCAGATAAAAAACAAC  
TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTAAACCTATT  
CCAGATGTAGTTCTTCCAATTAATATTTGAATAAATCTTTGTACTCAA

CGCGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG





## FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC  
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA  
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG  
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA  
TGAAATT CAGGTCTAGCTGGGTATTTATTCAGCAAAAAGGCTTGGAACCTCCCTTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCTTGAGTAAAT  
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA  
GCCCATATTTGATGAGTATTTTGGGTTGTGTGTAACCAATGAACATTTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTTATACCAAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATCTTAAAAA

## **FIGURE 34**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVVKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMEYEGDN SGPMTKFIQSAAPKSLLFMVITYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAETIQIEGCIPKERS

### **Signal sequence.**

amino acids 1-20

### **N-glycosylation sites.**

amino acids 120-124, 208-212

### **Glycosaminoglycan attachment site.**

amino acids 80-84

### **N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125